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ABSTRACT OF THE DISCLOSURE

Peaks are extracted in a certain range of starting points of signals from migration waveforms. The peaks are classified on the basis of signal strengths for obtaining signal strength ratios of four groups classified. Corresponding bases are allocated to the four groups classified for obtaining a matrix value from the signal strength ratios of peak waveforms of the respective base groups. Base sequence is determined with the matrix value. Thus, the matrix value can be obtained from actual sample migration without employing an exclusive reagent kit.